IN THE CLAIMS:

The text of all pending claims, (including withdrawn claims) is set forth below. Cancelled and not entered claims are indicated with claim number and status only. The claims as listed below show added text with <u>underlining</u> and deleted text with ~~strikethrough~~. The status of each claim is indicated with one of (original), (currently amended), (cancelled), (withdrawn), (new), (previously presented), or (not entered).

Please ADD new claims 34-36 and AMEND the claims in accordance with the following:

1. (currently amended) A method for ~~supporting a user in~~ predicting a gene expression site, the gene expression site being one of a cell, a tissue and an organ, said method comprising:

calculating a distance between a first gene and each of a plurality of second genes on a genome sequence, where the first gene is an unknown gene having an unknown gene expression site, while the second genes are known genes having known gene expression sites;

<u>extracting the gene expression sites of the second genes from an expression profile database;</u>

determining a first gene expression site, based on the distance, as a selected gene expression site of at least one of the second genes that has a predetermined distance relation with the first gene, the predetermined distance relation having been determined based on a sensitivity and a specificity<u> that define an upper limit of the distance</u>; and

outputting <u>on a display </u>the first gene expression site determined by said determining.

2. (previously presented) The method according to claim 1, wherein the distance is smaller than a predetermined threshold.

3. (previously presented) The method according to claim 1, wherein said calculating includes calculating a first distance between a start position of a target gene and a start position of the first gene, and a second distance between the start position of the target gene and a start position of the second gene on the genome sequence.

4. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the end position of the first gene and the end position of the second gene on the genome sequence.

5. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the start position of the first gene and the end position of the second gene on the genome sequence.

6. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the end position of the first gene and the start position of the second gene on the genome sequence.

7. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between first and second positions, the first position being between the start and end positions of the first gene on the genome sequence, and the second position being between the start and end positions of the second gene on the genome sequence.

8. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between a position between the start and end positions of the first gene and the start position of the second gene on the genome sequence.

9. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between a position between the start and end positions of the first gene and the end position of the second gene on the genome sequence.

10. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the start position of the first gene and a position between the start and end positions of the second gene on the genome sequence.

11. (withdrawn) The method according to claim 1, wherein the calculating includes calculating a distance between the end position of the first gene and a position between the start and end positions of the second gene on the genome sequence.

Claims 12-24 (cancelled)

25. (currently amended) A computer-readable medium encoded with a computer program, including computer executable instructions, for supporting a user in predicting a gene expression site, the gene expression site being one of a cell, a tissue and an organ, and the

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computer executable instructions, when executed by the computer, cause the computer to perform a method comprising:

calculating a distance between a first gene and each of a plurality of second genes on a genome sequence, where the first gene is an unknown gene having an unknown gene expression site, while the second genes are known genes having known gene expressions sites;

extracting the gene expression sites of the second genes from an expression profile database;

determining a first gene expression site of the first gene, based on the distance, as a selected gene expression site of at least one of the second genes that has a predetermined distance relation with the first gene, the predetermined distance relation having been determined based on a sensitivity and a specificity that define an upper limit of the distance; and

outputting on a display the first gene expression site as determined by said determining.

26. (previously presented) The computer program product according to claim 25, wherein the distance is smaller than a predetermined threshold.

27. (cancelled)

28. (currently amended) An apparatus for ~~supporting a user in~~ predicting a gene expression site, where the gene expression site is one of a cell, a tissue and an organ, said apparatus comprising:

a calculation unit that calculates a distance between a first gene and each of a plurality of second genes on a genome sequence, where the first gene is an unknown gene having an unknown gene expression site, while the second genes are known genes having known gene expression sites;

an extracting unit that extracts the gene expression sites of the second genes from an expression profile database;

a determination unit that determines a first gene expression site of the first gene, based on the distance, as a selected gene expression site of at least one of the second genes that has a predetermined distance relation with the first gene, the predetermined distance relation having been determined based on a sensitivity and a specificity that define an upper limit of the distance; and

~~an output~~ a display unit that ~~outputs~~ displays the first gene expression site determined by said determination unit.

29. (previously presented) The apparatus according to claim 28, wherein the distance is smaller than a predetermined threshold.

30. (cancelled)

31. (currently amended) The method according to claim 1, wherein when the first site and ~~the~~ a second site of the selected gene expression site of at least one of the second genes are identical, the second site is deleted from ~~the~~ a list before being output.

32. (previously presented) The method according to claim 1,
wherein the sensitivity is a ratio of predicted expression sites for an unknown gene to previously determined expression sites for the unknown gene determined by another method, and
wherein the specificity is a ratio of unpredicted expression sites for the unknown gene to non-expression sites for the unknown gene previously determined by the other method.

33. (currently amended) A method of ~~supporting a user in~~ determining a gene expression site, comprising:
calculating a distance of an unknown gene having an unknown gene expression site from each of a plurality of known gene expression sites for known genes on a genome sequence~~; and~~
extracting the gene expression sites for known genes from an expression profile database;
outputting on a display a predicted gene expression site of the unknown gene based on a sensitivity, a specificity and the distance calculated between the unknown gene and at least one of the known genes, the distance based on the sensitivity and the specificity which define an upper limit of the distance.

34. (new) The method according to claim 1, wherein the extracting includes weighting each of the gene expression sites based on the distance of the corresponding second gene relative to the first gene.

35. (new) The computer-readable medium according to claim 25, wherein the extracting includes weighting each of the gene expression sites based on the distance of the corresponding second gene relative to the first gene.

36. (new) The apparatus according to claim 28, wherein the extracting unit weights each of the gene expression sites based on the distance of the corresponding second gene relative to the first gene.